

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: GRAY, Joe W.  
COLLINS, Colin  
HWANG, Soo-In  
GODFREY, Tony  
KOWBEL, David  
ROMMENS, Johanna
- (ii) TITLE OF INVENTION: GENES FROM THE 20q13 AMPLICON AND THEIR  
USES
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Townsend and Townsend and Crew
  - (B) STREET: Two Embarcadero Center, 8th Floor
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/731,499
  - (B) FILING DATE: 16-OCT-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/680,395
  - (B) FILING DATE: 15-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Hunter, Tom
  - (B) REGISTRATION NUMBER: 38,498
  - (C) REFERENCE/DOCKET NUMBER: 23070-068910
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 576-0200
  - (B) TELEFAX: (415) 576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3000 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..3000
  - (D) OTHER INFORMATION: /note= "cDNA clone 3bf4 of 3kb  
transcript of tyrosine kinase gene A6"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGCCGGCCG	GGGCGCCTGG	CTGCACTCAG	CGCCGGAGCC	GGGAGCTAGC	GGCCGCCGCC	60
ATGTCCCACC	AGACCGGCAT	CCAAGCAAGT	GAAGATGTTA	AAGAGATCTT	TGCCAGAGCC	120
AGAAATGGAA	AGTACAGACT	TCTGAAAATA	TCTATTGAAA	ATGAGCAACT	TGTGATTGGA	180
TCATATAGTC	AGCCTTCAGA	TTCCTGGGAT	AAGGATTATG	ATTCTTTTGT	TTTACCCCTG	240
TTGGAGGACA	AACAACCATG	CTATATATTA	TTCAGGTTAG	ATTCTCAGAA	TGCCCAGGGA	300
TATGAATGGA	TATTCATTGC	ATGGTCTCCA	GATCATTCTC	ATGTTCGTCA	AAAAATGTTG	360
TATGCAGCAA	CAAGAGCAAC	TCTGAAGAAG	GAATTTGGAG	GTGGCCACAT	TAAAGATGAA	420
GTATTTGGAA	CAGTAAAGGA	AGATGTATCA	TTACATGGAT	ATAAAAAATA	CTTGCTGTCA	480
CAATCTTCCC	CTGCCCCACT	GACTGCAGCT	GAGGAAGAAC	TACGACAGAT	TAAAATCAAT	540
GAGGTACAGA	CTGACGTGGG	TGTGGACACT	AAGCATCAAA	CACTACAAGG	AGTAGCATTT	600
CCCATTTCTC	GAGAAGCCTT	TCAGGCTTTG	GAAAAATTGA	ATAATAGACA	GCTCAACTAT	660
GTGCAGTTGG	AAATAGATAT	AAAAAATGAA	ATTATAATTT	TGGCCAACAC	AACAAATACA	720
GAAGTGAAAG	ATTTGCCAAA	GAGGATTTCC	AAGGATTTCAG	CTCGTTACCA	TTTCTTTCTG	780
TATAAACATT	CCCATGAAGG	AGACTATTTA	GAGTCCATAG	TTTTTATTTA	TTCAATGCCT	840
GGATACACAT	GCAGTATAAG	AGAGCGGATG	CTGTATTCTA	GCTGCAAGAG	CCGTCTGCTA	900
GAAATTGTAG	AAAGACAACT	ACAAATGGAT	GTAATTAGAA	AGATCGAGAT	AGACAAATGGG	960
GATGAGTTGA	CTGCAGACTT	CCTTTATGAA	GAAGTACATC	CCAAGCAGCA	TGCACACAAG	1020
CAAAGTTTTG	CAAAACCAAA	AGGTCCTGCA	GGAAAAAGAG	GAATTCGAAG	ACTAATTAGG	1080
GGCCCAGCGG	AAACTGAAGC	TACTACTGAT	TAAAGTCATC	ACATTAAACA	TTGTAATACT	1140
AGTTTTTTTAA	AAGTCCAGCT	TTTAGTACAG	GAGAACTGAA	ATCATTCCAT	GTTGATATAA	1200
AGTAGGGAAA	AAAATTGTAC	TTTTTGGAAA	ATAGCACTTT	TCACTTCTGT	GTGTTTTTAA	1260
AATTAATGTT	ATAGAAGACT	CATGATTTCT	ATTTTTGAGT	TAAAGCTAGA	AAAGGGTTCA	1320
ACATAATGTT	TAATTTTGTC	ACACTGTTTT	CATAGCGTTG	ATTCCACACT	TCAAATACTT	1380
CTTAAAATTT	TATACAGTTG	GGCCAGTTCT	AGAAAGTCTG	ATGTCTCAAA	GGGTAAACTT	1440
ACTACTTTCT	TGTGGGACAG	AAAGACCTTA	AAATATTCAT	ATTACTTAAT	GAATATGTTA	1500
AGGACCAGGC	TAGAGTATTT	TCTAAGCTGG	AAACTTAGTG	TGCCTTGGAA	AAGCCGCAAG	1560
TTGCTTACTC	CGAGTAGCTG	TGCTAGCTCT	GTCAGACTGT	AGGATCATGT	CTGCAACTTT	1620
TAGAAATAGT	GCTTTATATT	GCAGCAGTCT	TTTATATTTG	ACTTTTTTTT	AATAGCATTA	1680
AAATTGCAGA	TCAGCTCACT	CTGAAACTTT	AAGGGTACCA	GATATTTTCT	ATACTGCAGG	1740
ATTTCTGATG	ACATTGAAAAG	ACTTTAAACA	GCCTTAGTAA	ATTATCTTTC	TAATGCTCTG	1800
TGAGGCCAAA	CATTTATGTT	CAGATTGAAA	TTTAAATTAA	TATCATTCAA	AAGGAAACAA	1860
AAAATGTTGA	GTTTTAAAAA	TCAGGATTGA	CTTTTTTCTC	CAAAACCATA	CATTTATGGG	1920
CAAATTGTGT	TCTTTATCAC	TTCCGAGCAA	ATACTCAGAT	TTAAAATTAC	TTTAAAGTCC	1980

TGGTACTTAA CAGGCTAACG TAGATAAACA CCTTAATAAT CTCAGTTAAT ACTGTATTTT	2040
AAAACACATT TAACTGTTTT CTAATGCTTT GCATTATCAG TTACAACCTA GAGAGATTTT	2100
GAGCCTCATA TTTCTTTGAT ACTTGAAATA GAGGGAGCTA GAACACTTAA TGTTTAATCT	2160
GTAAACCTG CTGCAAGAGC CATAACTTTG AGGCATTTTC TAAATGAACT GTGGGGATCC	2220
AGGATTTGTA ATTTCTTGAT CTAAACTTTA TGCTGCATAA ATCACTTATC GGAAATGCAC	2280
ATTTTCATAGT GTGAAGCACT CATTTCCTAAA CCTTATTATC TAAGGTAATA TATGCACCTT	2340
TCAGAAATTT GTGTTGAGT AAGTAAAGCA TATTAGAATA ATTGTGGGTT GACAGATTTT	2400
TAAAATAGAA TTTAGAGTAT TTGGGGTTTT GTTTGTTTAC AAATAATCAG ACTATAATAT	2460
TTAAACATGC AAAATAACTG ACAATAATGT TGCATTGTT TACTAAAGAT ATAAGTTGTT	2520
CCATGGGTGT ACACGTAGAC AGACACACAT ACACCCAAAT TATTGCATTA AGAATCCTGG	2580
AGCAGACCAT AGCTGAAGCT GTTATTTTCA GTCAGGAAGA CTACCTGTCA TGAAGGTATA	2640
AAATAATTTA GAAGTGAATG TTTTCTGTGA CCATCTATGT GCAATTATAC TCTAAATTCC	2700
ACTACACTAC ATTAAAGTAA ATGGACATTC CAGAATATAG ATGTGATTAT AGTCTTAAAC	2760
TAATTATTAT TAAACCAATG ATTGCTGAAA ATCAGTGATG CATTGTGTTAT AGAGTATAAC	2820
TCATCGTTTA CAGTATGTTT TAGTTGGCAG TATCATACCT AGATGGTGAA TAACATATTC	2880
CCAGTAAATT TATATAGCAG TGAAGAATTA CATGCCTTCT GGTGGACATT TTATAAGTGC	2940
ATTTTATATC ACAATAAAAA TTTTCTCTCT TTAAAAAAA AAAACAAGAA AAAAAAAAAA	3000

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 723 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: /note= "cDNA clone 1b11 of 3.5kb transcript"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGAAGCTGT CATGGTTACC GTCTCTAACG TTGGACTCTT AAGAAAATGA TTATTCCTGG	60
TTTCTAGACA GGCCAAATGT AATTCACCTA CGTGGCAGAT TAAAGAGGTG GGCTTACTAG	120
ATTTGATTGG GTATTGAGCA TGCTCTGAAT GACAGTCCCC AAAAAGGACC TCTTATCCGT	180
TCTTCCCCTT GGGGAAGGGC TTTTGCCACT TCCATGTCAA TGTGGCAGTT GAGCTTGGA	240
ATTGGTGCGT TGTACAACAT AAGCATTACT TCTCCAAGAT GTGCCTGTGT AGAAATGGTC	300
ATAGATTCAA AACTGTAGCT ACTATGTGGA CAGGGGGGCA GCAAGGACCC CACTTTGTAA	360

AACATGTTTT	GGGGGAATGT	TTTGTTTTTC	ATTTTCTTAT	TACCTGGCAA	AATAATCCAG	420
GTGGTGTGTG	AGTCACCACT	AGAGATTATA	AAGTCCAAGG	AAGTAGAATC	AGCCTTACAA	480
ACAGTGGACC	TCAACGAAGG	AGATGCTGCA	CCTGAACCCA	CWGAAGCGAA	ACTCAAAAGA	540
GAAGAAAGCA	AACCAAGAAC	CTCTCTGATG	RCGTTTCTCA	GACAAATGGT	AAGCCCCCTTA	600
CTTCCAGTAT	AGGAAACCTA	AGATACCTAG	AGCGGCTTTT	GGGAACAATG	GGCTCATGCC	660
ACAGGTAGTA	GGAGACATAA	TTGTAGCTGG	TGTGTATGGA	ATGTGAATGG	AATATGGATT	720
GCG						723

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1507
- (D) OTHER INFORMATION: /note= "cDNA clone cc49 of 6-7kb transcript with homology to C2H2 zinc finger genes"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAGGTTGCT	GGGATTGACT	TCTTGCTCAA	TTGAAACACT	CATTCAATGG	AGACAAAGAG	60
CACTAATGCT	TTGTGCTGAT	TCATATTTGA	ATCGAGGCAT	TGGGAACCCT	GTATGCCTTG	120
TTTGTGAAA	GAACCAGTGA	CACCATCACT	GAGCTTCCTA	AAAGTTTCGAA	GAAGTTAGAG	180
GACTATACAC	TTTCTTTTGA	ACTTTTATAA	TAAATATTTG	CTCTGGTTTTT	GGAACCCAGG	240
ACTGTTAGAG	GGTGAGTGAC	AGGTCTTACA	GTGGCCTTAA	TCCAACCTCA	GAAATTGCCC	300
AACGGAACCT	TGAGATTATA	TGCAATCGAA	AGTGACAGGA	AACATGCCAA	CTCAATCCCT	360
CTTAATGTAC	ATGGATGGCC	AAGAGTGATT	GGCAGCTCTC	TTGCCAGTCC	GATGGAGATG	420
GAGATGCCTT	GTCAATGAAA	GGGCCCNCTG	TTGTCAATTC	CGAGCTACAC	AAAGAAAAAA	480
ATGTCAATCC	GAATCGAGGG	GAATATGCCC	TTGGATTGCA	TGTTCTGCAG	CCAGACCTTC	540
ACACATTCAG	AAGACCTTAA	TAAACATGTC	TTAATGCAAC	ACCGGCCTAC	CCTCTGTGAA	600
CCAGCAGTTC	TTCGGGTTGA	AGCAGAGTAT	CTCAGTCCGC	TTGATAAAAG	TCAAGTGCGA	660
ACAGAACCTC	CCAAGGAAAA	GAATTGCAAG	GAAAATGAAT	TTAGCTGTGA	GGTATGTGGG	720
CAGACATTTA	GAGTCGCTTT	TGATGTTGAG	ATCCACATGA	GAACACACAA	AGATTCTTTT	780
ACTTACGGGT	GTAACATGTG	CGGAAGAAGA	TTCAAGGAGC	CTTGGTTTCT	TAAAAATCAC	840
ATGCGGACRC	ATAATGGCAA	ATCGGGGGCC	AGAAGCAAAC	TGCAGCAAGG	CTTGGAGAGT	900
AGTCCAGCAA	CGATCAACGA	GGTCGTCCAG	GTGCACGCGG	CCGAGAGCAT	CTCCTCTCCT	960

TGCAAAATCT	GCATGGTTTG	TGGCTTCCTA	TTTCCAAATA	AAGAAAGTCT	AATTGAGCAC	1020
CGCAAGGTGC	ACACCAAAAA	AACTGCTTTC	GGTACCAGCA	GCGCGCAGAC	AGACTCTCCA	1080
CAAGGAGGAA	TGCCGTCCTC	GAGGGAGGAC	TTCCTGCAGT	TGTTCAACTT	GAGACCAAAA	1140
TCTCACCTG	AAACGGGGAA	GAAGCCTGTC	AGATGCATCC	CTCAGCTCGA	TCCGTTTACC	1200
ACCTTCCAGG	CTTGGCAKCT	GGCTACCAAA	GGAAWAGTTG	CCATTTGCCA	AGAAGTGAAG	1260
GAATTGGGGC	AAGAAGGGAG	CACCGACAAC	GACGATTCTGA	GTTCCGAGAA	GGAGCTTGGA	1320
GAAACAAATA	AGAACCATTG	TGCAGGCCTC	TCGCAAGAGA	AAGAGAAGTG	CAAACACTCC	1380
CACGGCGAAG	CGCCCTCCGT	GGACGCGGAT	CCCAAGTTAC	CCAGTAGCAA	GGAGAAGCCC	1440
ACTCACTGCT	CCGAGTGC GG	CAAAGCTTTC	AGAACCTACC	ACCAGCTGGT	CTTGCACTCC	1500
AGGGTCC						1507

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2605
- (D) OTHER INFORMATION: /note= "cDNA clone cc43 of 4 kb transcript"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAGCTCGAA	ATTAACCCTC	ACTAAAGGGA	ACAAAAGCTG	GAGCTCCACC	GCGGTGGCGG	60
CCGCTCTAGA	ACTAGTGGAT	CCCCCGGGCT	GCAGGAATTC	GGCACGAGCT	GGGCTACTAC	120
GATGGCGATG	AGTTTCGAGT	GGCCGTGGCA	GTATCGCTTC	CCACCCTTCT	TTACGTTACA	180
ACCGAATGTG	GACACTCGGC	AGAAGCAGCT	GGCCGCCTGG	TGCTCGCTGG	TCCTGTCCTT	240
CTGCCGCCTG	CACAAACAGT	CCAGCATGAC	GGTGATGGAA	GCTCAGGAGA	GCCCGCTCTT	300
CAACAACGTC	AAGCTACAGC	GAAAGCTTCC	TGTGGAGTCG	ATCCAGATTG	TATTAGAGGA	360
ACTGAGGAAG	AAAGGGAACC	TCGAGTGGTT	GGATAAGAGC	AAGTCCAGCT	TCCTGATCAT	420
GTGGCGGAGG	CCAGAAGAAT	GGGGGAAACT	CATCTATCAG	TGGGTTTCCA	GGAGTGGCCA	480
GAACAACTCC	GTCTTTACCC	TGTATGAACT	GACTAATGGG	GAAGACACAG	AGGATGAGGA	540
GTTCCACGGG	CTGGATGAAG	CCACTCTACT	GCGGGCTCTG	CAGGCCCTAC	AGCAGGAGCA	600
CAAGGCCGAG	ATCATCACTG	TCAGCGATGG	CCGAGGCGTC	AAGTTCTTCT	AGCAGGGACC	660
TGTCTCCCTT	TACTTCTTAC	CTCCACCTT	TCCAGGGCTT	TCAAAAGGAG	ACAGACCCAG	720
TGTCCCCCAA	AGACTGGATC	TGTGACTCCA	CCAGACTCAA	AAGGACTCCA	GTCCTGAAGG	780

CTGGGACCTG	GGGATGGGTT	TCTCACACCC	CATATGTCTG	TCCCTTGGAT	AGGGTGAGGC	840
TGAAGCACCA	GGGAGAAAAT	ATGTGCTTCT	TCTCGCCCTA	CCTCCTTTCC	CATCCTAGAC	900
TGTCCTTGAG	CCAGGGTCTG	TAAACCTGAC	ACTTTATATG	TGTTACACACA	TGTAAGTACA	960
TACACACATG	CGCCTGCAGC	ACATGCTTCT	GTCTCCTCCT	CCTCCCACCC	CTTTAGCTGC	1020
TGTTGCCTCC	CTTCTCAGGC	TGGTGCTGGA	TCCTTCCTAG	GGGATGGGGG	AAGCCCTGGC	1080
TGCAGGCAGC	CTTCCAGGCA	ATATGAAGAT	AGGAGGCCCA	CGGGCCTGGC	AGTGAGAGGT	1140
GTGGCCCCAC	ACCGATTAT	GATATTAAAA	TCTCAACTCC	CAAAAAAAAAA	AAAAAAAAAAA	1200
CTGAGACTAG	TTCTCTCTCT	CTCGAGAACT	AGTCTCGAGT	TTTTTTTTTTT	TTTTTTTTTTT	1260
TTTTTTTTTTT	TTTTTTTTTTG	GCTTTAAGGA	TTTATTTATT	GTTTCCTCTT	TACAGTGTCC	1320
ACTTTTCTCT	ACTTAATACT	ACTTTCCAGT	CTCAGAAGCC	CAGAGGGAAA	AAAAAAGAC	1380
CATGAATCTT	CCTCTCCCAG	ATTAAAGTAC	ACACTTTGGA	AAACAGATTG	GAAAACCTTT	1440
CTGAAAAAAG	TTGACTGAAA	CTCCAAACCA	ACATGCCATA	TTGTTGATGT	TGCTCATGAA	1500
AATTGTTAAA	AACCTGTTCT	AGATAAAGAA	CAGTCTCAAG	TTTTTGTACA	GCCTACACAT	1560
AGTACAAGGG	TCCCTATGA	TGATTCTTCT	GTAGGACGAA	ATAATGTAAT	TTTTTCAGTT	1620
TCTGGTTTAT	AACTCTCTCG	ATCTCAGAGT	TGACTGATTA	AAACACCTAC	TCATGCAACA	1680
GAGAATAAAG	CACTCATATT	TTTATAAATT	ATATGGACCA	AACTATTTTG	GAAATCTTAT	1740
CTATTGGAGA	CACAATATGC	TGGACTAAAG	CAATAATTAT	TTTATTCTCA	ATGTCTGTGC	1800
TAACCTCAAT	GACTTAGAAT	GCTTTGCTAT	ATTTTGCCTC	TATGCCTCAA	CCACACTGGC	1860
TTTCTTTTAG	CTCTTGAACA	AGCCAAACTG	CTTCCTGCCT	CAGGACCAGA	TATTTTGGGA	1920
CTTCTCTTAA	GAATTCTATT	TCCTTAATTC	TTTATCTGGG	TAACTTAGTT	TTATCCAACA	1980
CTTCAGATCC	TGCCGTAAAA	ACTCTTCTTA	TAGAAGCCTG	TCATGACACT	GTCTCTCTTC	2040
TCCAACATAC	TCACCAGCAC	ACATGTAGAC	TAGATTAGAA	CCTCCTGTTT	TTCTTTTTTCA	2100
TACTTTTCTC	TATCATGCTT	CCCTCCATTA	TAATATTTTT	ATTATGTGTG	TGAATGTCTG	2160
CCCCAAGTCA	GTTTCCTCAC	TAAACTATAA	ACTCCGTAAA	GCTGGGATCC	TTCCAATTTT	2220
GATCACCCT	TAGTACAGTA	GGAACACAGT	AAAGATTCAA	TTGGTATTTG	TGGAATGAAT	2280
GAATGAATTG	TTTTGCTAGT	AAAGTCTGGG	GGAACCCAGG	TGAGAAGAGC	CTAGAAAGCA	2340
GGTCGAATCC	AAGGCTAGAT	AGACTTAGTG	TTACTCAAGA	AAGGGTAGCC	TGAAAATAAA	2400
GGTTCAAATT	ATAGTCAAGA	ATAGTCAAGA	CATGGGCAAG	ACAAGAGTGC	TGCTCGTGCC	2460
GAATTGATA	TCAAGCTTAT	CGATACCGTC	GACCTCGAGG	GGGGGCCCGG	TACCCAATTC	2520
GCCCTATAGT	GAGTCGTATT	ACAATTCCT	GGCCGTCGTT	TTACAACGTC	GTGACTGGGA	2580
AAACCCTGGC	GTTACCCAAC	TTAAT				2605

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1288 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -  
 (B) LOCATION: 1..1288  
 (D) OTHER INFORMATION: /note= "cDNA clone 41.1 with homology  
 to homeobox T shirt gene from  
 Drosophila"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGGGCAGCG AGAAGGAGAA ACCCCAGCCC CTGGAGCCCA CATCTGCTCT GAGCAATGGG	60
TGCGCCCTCG CCAACCACGC CCCGGCCCTG CCATGCATCA ACCCACTCAG CGCCCTGCAG	120
TCCGTCCTGA ACAATCACTT GGGCAAAGCC ACGGAGCCCT TGCGCTCACC TTCCTGCTCC	180
AGCCCAAGTT CAAGCACAAT TTCCATGTTT CACAAGTCGA ATCTCAATGT CATGGACAAG	240
CCGGTCTTGA GTCCTGCCTC CACAAGGTCA GCCAGCGTGT CCAGGCGCTA CCTGTTTGAG	300
AACAGCGATC AGCCCATTGA CCTGACCAAG TCCAAAAGCA AGAAAGCCGA GTCCTCGCAA	360
GCACAATCTT GTATGTCCCC ACCTCAGAAG CACGCTCTGT CTGACATCGC CGACATGGTC	420
AAAGTCCTCC CCAAAGCCAC CACCCCAAAG CCAGCCTCCT CCTCCAGGGT CCCCCCATG	480
AAGCTGGAAG TGGATGTCAG GCGCTTTGAG GATGTCTCCA GTGAAGTCTC AACTTTGCAT	540
AAAAGAAAAG GCCGGCAGTC CAACTGGAAT CCTCAGCATC TTCTGATTCT ACAAGCCAG	600
TTTGCTCTGA GCCTCTTCCA GACATCAGAG GGCAAATACC TGCTGTCTGA TCTGGGCCCA	660
CAAGAGCGTA TGCAAATCTC TAAGTTTACG GGAATCTCAA TGACCACTAT CAGTCACTGG	720
CTGGCCAACG TCAAGTACCA GCTTAGGAAA ACGGGCGGGA CAAAATTTCT GAAAAACATG	780
GACAAAGGCC ACCCATCTT TTATTGCAGT GACTGTGCCT CCCAGTTCAG AACCCCTTCT	840
ACCTACATCA GTCACCTAGA ATCTCACCTG GGTTCCTCAA TGAAGGACAT GACCCGCTTG	900
TCAGTGGACC AGCAAAGCAA GGTGGAGCAA GAGATCTCCC GGGTATCGTC GGCTCAGAGG	960
TCTCCAGAAA CAATAGCTGC CGAAGAGGAC ACAGACTCTA AATTCAAGTG TAAGTTGTGC	1020
TGTCGGACAT TTGTGAGCAA ACATGCGGTA AAATCCACC TAAGCAAAAC GCACAGCAAG	1080
TCACCCGAAC ACCATTCACA GTTTGTAACA GACGTGGATG AAGAATAGCT CTGCAGGACG	1140
AATGCCTTAG TTTCCACTTT CCAGCCTGGA TCCCCTCACA CTGAACCCTT CTTCGTTGCA	1200
CCATCCTGCT TCTGACATTG AACTCATTGA ACTCCTCTG ACACCCTGGC TCTGAGAAGA	1260
CTGCCAAAAA AAAAAAAAAA AAAAATTC	1288

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2821 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..2821  
(D) OTHER INFORMATION: /note= "cDNA clone GCAP encodes a  
guanino cyclase activating protein  
(GCAP) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATCCTAAGAC GCACAGCCTG GGAAGCCAGC ACTGGGGAAG TGGTGCTGAG GGATGTGGGT	60
CACTGGGGTG AAGGTGGAGC TTTCAGGGTC TCCCGTCAAT GCAGCTGAGT TTTCTTTGGC	120
AGGGAATTTA CCAGCTGAAG AAAGCCTGCC GGCGAGAGCT ACAAAGTGAAG CAAGGCCAGC	180
TGCTCACACC CGAGGAGGTC GTGGACAGGA TCTTCCTCCT GGTGGATGAG AATGGAGATG	240
GTAAGAGGGG CAGAGATGGG GAGAGTGCTG TCCACTCTGC ATCATCGCCA CTTTCTGGCC	300
GCACGTCTTT GGGCAAGGCC CTCCACCTTC CAACCCTGGG GTCCTCATCT GTGAGAAGGC	360
TGTGGAGAAG ATGTCATGAA CTAACAAAGG GACTCATGAG CACGTGTTTG TAGGAGTGAC	420
TAAAAGTCCT ACAGGAGTTG CTGATGGAGG CCAGGCACGC AGAATAGAAA GAATAGGAAC	480
TTTGGAGTCA GGCAGGGAGT GATATATTGA GCTTCTCGTC CTAGTCTCAA TTTCTTCATC	540
TGGAATATGG GGATAATAAT AGTGGTTGAG AGGAATGAAT AGGATAATGT GTTTAAGAGC	600
AGGCATAGGG TAGACCTCCA TTCAGGCTGC TTGGGCTTTC CTCCCTGTAG CCCAAAGCCC	660
AGCCTCAGGG CTATGTGGGG AGAGAGCTGG CTTGGAATAC ACACTTGAGC CCTCCAGCTC	720
TCTCAGCTCC ACCCAGCATT TCCGTGGTAC CATGCGCAAA AGTAAACTT CAATTCATCA	780
GCAAAGAAAG CCCCTTAAAG GTGGCAGGAG ACTCCTGGAG ATTCAGACAC CTGACAAGCC	840
GCAAGCTTGA GGTCTGAGAC TGCAGGATAG TTGGCATAAG ACGTGTAGGC GCATCCTGGG	900
AGCGAGGTCT CTCTCTCTGC CCCAGACCC AGGTCTCCCC TTCTTCTACA TGACCACCTC	960
TCCTCCCCCT TGCTCAGGCC AGCTGTCTCT GAACGAGTTT GTTGAAGGTG CCCGTCGGGA	1020
CAAGTGGGTG ATGAAGATGC TGCAGATGGA CATGAATCCC AGCAGCTGGC TCGCTCAGCA	1080
GAGACGGAAG AGTGCCATGT TCTGAGGAGT CTGGGGCCCC TCCACGACTC CAGGCTCACC	1140
CAGGTTTCCA GGGTAGTAGG AGGGTCCCCT GGCTCAGCCT GCTCATGCCC ACTCTTCCCC	1200
TGGTGTTGAC TTCCTGGCAC CCCCTGTGCA GGGCTGAGTG GGGATGGGGA AGGGCTGCTG	1260
GGTTTGAAGT GGCCAACAGG GCATAGTCCA TTTTGGAGGA GTCCCTGGGA TGGTGAAGGG	1320
AATTCAGTTA CTTTTCTGTG TCAGCCGCTC CTGGGAGGAC TGTGCCTTGG CTGGGTGGTT	1380
GTGGGGCTCC CACAGTTTCT GGGTGTTCTC AGTTGGAAGC AAGAGCCAAC TGAGGGGTGA	1440
GGGTCCCACA GACCAAATCA GAAATGAGAA CACAAAGACT GGTAGGAGGC AGGGGTGGGA	1500
GGGTGTTGAG ACTGAAGAAA AGGCAGGAGT TGCCGGGCAC GGTGGCTCAC GCCTGTAATC	1560



CCAGCACTTT	GGGAGGCCGA	GGCGGGCAGA	TCACGAGGTC	AGGAGATCGA	GACCATCCTG	1620
GCTAACACGG	GGTGAAACCC	CGTCTCTACT	AAAAATACAA	AAAATCAGCC	GGGTGAGGTG	1680
GCGGGCGCCT	GTAGTCCCAG	CTACTCAGGA	GGCTGAGGCA	AGAGAATGGC	GTGAACCCCA	1740
GGGGGCCGAG	CCTACAGTGA	GCCGAGATTG	CGCCACTGCA	CTCCAGCCTG	GACGACAGTG	1800
AGACTCCGTC	TCAAAAAAAAA	AAAAAGAAAG	AAAAGAAAAG	GCAGGAGTTT	TGGGGGGCAG	1860
GGGGCAGCAA	TAATTCTATA	ACTTCCGGGA	TGCTGAGGGG	CGTTCATGGG	GAGGACCCTG	1920
GCCTCCTCCT	CCCCAAGGCA	TCCTCACCAG	TGGTGTCAAC	AGGAAAAATG	GCAGCAAATA	1980
CGCTGCAGGC	TGTGGTCTTT	CTGCCCTTTGA	AAGGGTCAGC	TGTACTTAAA	GGGACTGTTT	2040
CAGCTCTGCC	TGGGTGCTGC	TCTGGGACCC	CCTGCTGCCA	ACCCACCACT	CCCCCAACAA	2100
TCCTCTCTTT	CCATCCATAT	CCCCCAGTAT	GGACCTTCCA	CAACTCCCAG	CCATAAGCTG	2160
AATGTTTCTC	TTTAAAGGAT	GGAGAAAAC	TCTGTCTGTC	TCTGGCAAGA	ATTGGGGGAC	2220
TGTTGACTGG	GATTGTGGGC	TGGGCTTGCC	TTCTAACTGC	TGTGTGACCC	AAGACAGCCA	2280
CTTCTCCTCC	CTAACCTTGG	TTATGTCTTG	GCAGCACAGT	GAGCAGGTCG	GACTIONGCGA	2340
ACAGTTTTGG	ATTATTGTGT	TTTTAGATGT	GGAATTATTT	TTTGTATAT	AAACTCTTAT	2400
GTGTAACCCC	AATATAGAAA	CTAGATTAAA	AGGGAGTCTC	TCTGGTTGAA	AGGGGAGCTG	2460
AGTACCCTCT	GGAACCTGGAG	GCACCTCTGA	AAAAAGCAAA	CTGAAAACCA	GTGCCCTGGG	2520
TCACTGTTAC	TCCTATAAGA	CAGTTTAAAG	TGAGACCTGG	AAAAACATTT	GCTTTACCTT	2580
GAATAGATAG	GTTTTTATGT	TGGTATATAA	GAAATAAAAC	TAACCTATTA	ACCCTGAGAC	2640
TTTACAGGTG	TGTTATTTCA	TATGATAGTC	ATATAAAATT	TCCTTTAGAC	ATCAATTTTA	2700
GGTAAAAAAT	AATTGATTAG	AAAAATATTG	GCCAGGTGCA	GCAGCTCACA	CCTGCAATCC	2760
CAGGACTTTG	GGAGGCCGAG	GCGGGTGGAT	CACCTGAGGT	CAGGGGTTCA	AGACCAGCCT	2820
G						2821

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1205
- (D) OTHER INFORMATION: /note= "cDNA clone 1b4 for a serine threonine kinase"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGCGTGA	GTCCGCCCCC	CCAGTCACGT	GACCGCTGAC	TCGGGGCGTT	CTCCACTATC	60
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GCTTACCTAC CTCCCTCTGC AGGAACCCGG CGATATGGCT GCCGCTGTGC CCCGCGCCGC	120
ATTTCTCTCC CCGCTGCTTC CCTTCTCCTG GGCTTCCTGC TCCTCTCCGC TCCGCATGGC	180
GGCAGCGGCC TGCACACCAA GGCGCCCTTC CCCTGGATAC GGTCACTTTC TACAAGGTCA	240
TTCCCAAAG CAAGTTCGTC TGGTGAAGTT CGACACCCAG TACCCCTACG GTGAGAAGCA	300
GGATGAGTTC AAGCGTCTTC TGAAAACCTCG GCTTCCAGCG ATGATCTCTT GGTGGCAGAG	360
GTGGGGATCT CAGATTATGT GACAAGCTGA ACATGGAGCT GAGTGAGAAA TACAAGCTGG	420
ACAAAGAGAG CTACCCATCT TCTACCTCTT CCGGGATGGG GACTTTGAGA ACCCAGTCCC	480
ATACACTGGG GCAGTTAGGT TGGAGCCATC CAGCGCTGGC TGAAGGGGCA AGGGGTCTAC	540
CTAGGTATGC CTGGTGCCTG CCTGTATACG ACGCCCTGGC CGGGGAGTTC ATCAGGGCCT	600
CTGGTGTGGA GGCCGCCAGG CCCTCTTGAA GCAGGGGCAA GATAACCTCT CAAGTGTGAA	660
GGAGACTCAG AAGAGTGGGC CGAGCAATAC CTGAAGATCA TGGGGAAGAT CTTAGACCAA	720
GGGGAGCACT TCCAGCATCA GAGATGACAC GGATCGCCAG GCTGATTGAG AAGAACAAGA	780
TGAGTGACGG CAGAAGGAGG AGCTCCAGAA GAGCTTAAAC ATCCTGACTG CCTTCCAGAA	840
GAAGGGGGCC GAGAAAGAGG AGCTGTAAAA AGGCTGTCTG TGATTTTCCA GGGTTTGGTG	900
GGGGTAGGGA GGGGANAGTT AACCTGCTGG CTGTGANTCC CTTGTGGAAT ATAAGGGGGY	960
MSKGGGAAAA GWGGTACTAA CCCACGATTC TGAGCCCTGA GTATGCCTGG ACATTGATGC	1020
TAACATGACC ATGCTTGGGA TGTCTCTAGC TGGTCTGGGG ATAGCTGGAG CACTTACTCA	1080
GGTGGCTGGT GAAATGACAC CTCAGAAGGA ATGAGTGCTA TAGAGAGGAG AGAGGAGTGT	1140
ACTGCCCAGG TCTTTGACAG ATGTAATTCT CATTCAATTA AAGTTTCAGT GTTTTGGTTA	1200
AGTGG	1205

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: /note= "cDNA clone 20sa7 for a homolog of rat gene BEM-1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAAATCAGAA GTTTAATATG ACACAATTAA ATATATTTGT ATATCTCACA CCGGAGNTTC	60
TCTTCAAACA TAAGGAGTTA GAAATTACAA GTAGGCATAT GCTTCCTATA TTCAGATAAA	120
TTCATTTTCA TTAATTAAAT TCCAGATAGA GAGAAGTAAT TTTCGGAAAA GAAATGATAG	180

CTATATTAAA GCAGATATTC ATTACAATAC CATGTAGAGA CATAAGCAAT ATTTTGGCAT	240
CATTCTGTCC GCTCAGTAGG CCGTGTTCCT TCTGGTAGGG CCTTTGGAGA GTACCATCTA	300
TCTAAGATGG AGGAATGCTG TGGGAAGGGC GGGATGGAGG TGCCTTTTCT ACGCTGAACC	360
CCACACAGGA AATCTGCAGC CCACACAGCT GCCTCTGCGC CGCCTTCCAT GTGATCATCC	420
TGGTCAATGA AGTGAATTGT CCTATTTTCNG GGGGT	455

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..10365
- (D) OTHER INFORMATION: /note= "Genomic Sequence Encoding ZABC1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCATATT TCTTATTTTT TTGGGCGGAG AGGGGAGACT TGCTCTGTTG CCCAGGCTGG	60
ACCAGTGGTG CGATCTTGGC TCACTGCAAC CTCCACCTCC TGGGTTCAAG TGATTCCCAA	120
ATAGCTGGGA TTACAGGTGT GTATTACCAT GCCCAGCTAA TTTTGTATT TTTAGCAGAT	180
AAGGGGTTTC ACCATGTTGG CCAGGCTGGT CTCCAACCTCC TGGCCTCATG TGATCCACCC	240
ACTTCGGCTT CCCAAAGCAT TGGGAGTATA GGTGTGAGCC ACTATACCCG TCCTCACATC	300
ATATTTCTAA TCCCGAGACT GTAGAGCTGG TGTCTCTTTT TCTAAAGGAT GTCAGTAGAG	360
AAGTGGAGTT CCCCAAAATT ACAGTTTCAC GTATTAGTCA AGTTTCTAAA ATACAGTAAT	420
AATGTTGAGA GCTGACATAG GGACTAACTT GGTTTTTTTT TTTTTTTTTT TTTTCAAAT	480
TCTCACTGAA CTTTGATTTT GCTAAATAAG GACATTAAAA AAAAAACCAA AAAACTCCAC	540
TATTGCCTAT TGCCACTATT TGATTTTTTA AAAAATAAGC GTATTTTAGC ATCTAAAAGT	600
AGGAAGGACC TCAAATAAAT GAGTCTTTGT TCTTGGCCAG GGAAAACAGC GTTGTCAGAA	660
TTTGATAACT GTTTTTCTAG GGTATGTGCT GTTATTCAGT TAAAACCTTG CCTGGGACGC	720
TAGCATTCAG TAAATACTTG TTGAATAAGC AAATGAACT TAAGCTTCTA TGTATAGAAA	780
CCTAAGTCAC TTCACATTCT GATTAGCAGA GTAATTGAAT ATTCTTTTCA ATGTGTAGCT	840
CTATCCCCAG AACCACAGAA TATTGGAAC GTAAAGGCCA TCCTATAGTT TAACCAACTG	900
CGTTAAATAG ATAATAGAAA GATGTGGTAT GTGGCAGTGA CAACTTGAAG GTTGTGACTA	960
GAACTCGGGT CTCTGGAGTG TTCTATTATA TCACACCAAG CTGGTCACCA GCCCATGTGT	1020
TGATCCTCCA TTGTGATAGC AACAAAGAAA AGACTTCAGG ACATTCTTTC CTTTACCCTA	1080

ATCCTTGATC	TGCAGTCTTA	TTTAGAAAAG	CTTAATGTTA	AAGATCTAGT	TTATTCAAAA	1140
CTAAAGATAA	CAAGGAGTAT	GAGAATTTCT	ATTTCCGGAGT	GTAAAGGAGG	AGATGTTTCC	1200
TTGGCTTCTC	TGAGCCTGCA	GGCCTTCCTT	GCTCTTTAAG	GAAGTAGAGA	GAGGGAGGAA	1260
AGTAAAGTAT	GCTTTTGTTT	TTTAAGGTTA	CTTTGCTGGG	AGTAGTTTGC	ATGCCTTTTG	1320
GTTTTCTTGG	GTGGAATTAA	CTGACTTAAG	TTTTAAGTAG	TTGGGACTAT	TTAAAAACAA	1380
TGCCTATCCA	ATGTTTGCCA	TAAAGGCAGA	GGGTATTGGC	TTTAGAAGTT	AATTCTTCTC	1440
CAGGAGTGAA	AATTAGCTTC	TAAACCAGAA	GCAGCAGAGC	TAAATAAAGT	AATTTTCCAC	1500
CTGGCCAGTG	CATGATGTGA	AAGGTAGATT	AAAAAATGA	GAGGGCCCAT	TTTCTGATGA	1560
AAGACTAAGC	CATGTTGAAA	CAGCCCTGTT	GAGGATTTTA	TTTTAAATCT	ATACATTCCAC	1620
AAAGGAGCTT	TGTGTATGTC	TTTCCCTATT	TGTTGTTTGG	ACTAGGAAGC	CCCACCCAGT	1680
GCTTGTTGAA	GGCAGAAAGT	CGTTGAAAGC	AAGCTGGGAT	TTGAACAGTG	GATTGAGGTT	1740
TCGAATATCC	AGTGAACCAA	AATATATCAG	GGTTCCCCTG	GCCAAGATGA	GTGACCATTC	1800
TGAGGTGTTA	AGTATTTCTT	GAATGGGGAT	TTTAGGAAAA	GTTTCTGTAT	TTCTGTGCTC	1860
ATTTTGTTGA	CCTCTGTATG	TGCAAAATCT	CTAAGGGGGT	GTTTGGGCAC	TTAGATTTCT	1920
TGGATGCAGA	TTTGTTTGTA	TATGAAACAA	ATTTTAAATT	GTTTTGTATA	CACTGGATTT	1980
AAAATAGTTT	ACTAAAGTGT	TTTAATTTTT	TCATCTTAAT	TTTCACAGTT	CTTATAGTCT	2040
TTAGATTTAG	GGAGGCTGTT	GATGGCATCC	ACATGTGCAT	TTTAGTGGCA	TTTAAATGT	2100
ATTCAGCTGA	ATTTAACAAT	TCTGACCTA	AACTTGACA	TTTAGATTT	AAGTCGGTAA	2160
AGCACTGATT	TAAACTGGAT	TTTAACTGGA	TGAAATTCTG	ATTTAATAAG	TGTA CTGACT	2220
GGATAAAATG	CCAATGATTT	AATTAACAAG	CACGTTTAAC	AGGATGCCCT	ATATATTAGT	2280
TAAAAGTGAA	GCAATTGAAT	TAGGTACCTT	CTCTGCTGCG	TGAAAAAGAC	CGTATGACTC	2340
ACCCACACCA	GCCTTCTCTT	CGCTCTGAGT	GTAGCTAACC	GTTTCTGTTT	TTTTTCCTCT	2400
AGGGTTTGGA	AATCCCTTGT	CTCCAGGTTG	CTGGGATTGA	CTTCTTGCTC	AATTGAAACA	2460
CTCATTCAAT	GGAGACAAAG	AGAACTAATG	CTTTGTGCTG	ATTCATATTT	GAATCGAGGC	2520
ATTGGGAACC	CTGTATGCCT	TGTTTGTGGA	AAGAACCAGT	GACACCATCA	CTGAGCTTCC	2580
TAAAAGTTCT	AAGAAAGTTAG	AGGACTATAC	ACTTTCTTTT	GAACTTTTAT	AATAAATATT	2640
TGCTCTGGTT	TTTGGAACCC	AGGGCTGTTA	GAGGGGTGAG	TGACAAGTCT	TACAAGTGGC	2700
CTTATTCCAA	CTCCAGAAAT	TGCCCAACGG	AACTTTGAGA	TTATATGCAA	TCGAAAGTGA	2760
CAGGAAACAT	GCCAACTCAA	TCCCTCTTAA	TGTACATGGA	TGGGCCAGAA	GTGATTGGCA	2820
GCTCTCTTGG	CAGTCCGATG	GAGATGGAGG	ATGCCTTGTC	AATGAAAGGG	ACCGCTGTTG	2880
TTCCATTCCG	AGCTACACAA	GAAAAAATG	TCATCCAAAT	CGAGGGGTAT	ATGCCCTTGG	2940
ATTGCATGTT	CTGCAGCCAG	ACCTTCACAC	ATTCAGAAGA	CCTTAATAAA	CATGTCTTAA	3000
TGCAACACCG	GCCTACCCTC	TGTGAACCAG	CAGTTCTTCG	GGTTGAAGCA	GAGTATCTCA	3060
GTCCGCTTGA	TAAAAGTCAA	GTGCGAACAG	AACCTCCCAA	GGAAAAGAAT	TGCAAGGAAA	3120

ATGAATTTAG	CTGTGAGGTA	TGTGGGCAGA	CATTTAGAGT	CGCTTTTGAT	GTTGAGATCC	3180
ACATGAGAAC	ACACAAAGAT	TCTTTCACCT	ACGGGTGTAA	CATGTGCGGA	AGAAGATTCA	3240
AGGAGCCTTG	GTTTCTTAAA	AATCACATGC	GGACACATAA	TGGCAAATCG	GGGGCCAGAA	3300
GCAAACCTGCA	GCAAGGCTTG	GAGAGTAGTC	CAGCAACGAT	CAACGAGGTC	GTCCAGGTGC	3360
ACGCGGCCGA	GAGCATCTCC	TCTCCTTACA	AAATCTGCAT	GGTTTGTGGC	TTCCTATTTT	3420
CAAATAAAGA	AAGTCTAATT	GAGCACCGCA	AGGTGCACAC	CAAAAAAACT	GCTTTCGGTA	3480
CCAGCAGCGC	GCAGACAGAC	TCTCCACAAG	GAGGAATGCC	GTCTCGAGG	GAGGACTTCC	3540
TGCAGTTGTT	CAACTTGAGA	CCAAAATCTC	ACCCTGAAAC	GGGAAGAAG	CCTGTCAGAT	3600
GCATCCCTCA	GCTCGATCCG	TTCACCACCT	TCCAGGCTTG	GCAGCTGGCT	ACCAAAGGAA	3660
AAGTTGCCAT	TTGCCAAGAA	GTGAAGGAAT	CGGGGCAAGA	AGGGAGCACC	GACAACGACG	3720
ATTTCGAGTT	CGAGAAGGAG	CTTGGAGAAA	CAAATAAGGG	CAGTTGTGCA	GGCCTCTCGC	3780
AAGAGAAAGA	GAAGTGCAAA	CACTCCCACG	GCGAAGCGCC	CTCCGTGGAC	GCGGATCCCA	3840
AGTTACCCAG	TAGCAAGGAG	AAGCCCCTC	ACTGCTCCGA	GTGCGGCAAA	GCTTTCAGAA	3900
CCTACCACCA	GCTGGTCTTG	CACTCCAGGG	TCCACAAGAA	GGACCGGAGG	GCCGGCGCGG	3960
AGTCGCCCAC	CATGTCTGTG	GACGGGAGGC	AGCCGGGGAC	GTGTTCTCCT	GACCTCGCCG	4020
CCCCTCTGGA	TGAAAATGGA	GCCGTGGATC	GAGGGGAAGG	TGGTTCTGAA	GACGGATCTG	4080
AGGATGGGCT	TCCCGAAGGA	ATCCATCTGG	GTAAGCTGCC	CTGTCTCCGT	CCCGTGCTGT	4140
TCCGCCTGTG	TCTGTCTGTC	TCCCCGTCTC	CCCCTCTCTA	TTCCCATCTC	CAGACAACGC	4200
TGGCCAGGAA	TGGGGTTTGG	AGAGCCAGAG	TCAAGTCCAG	GCTCTTTTGT	GTATCACTCT	4260
GTGTAAGTCA	TTTAACCTCT	CAGGGCCTTA	ATTTTCTCAT	TTCTGTAATA	ACAGGGTTGA	4320
GTTAAGAGGT	CTCCTTGTTT	TGAAAATATA	TATATATTTT	TTAAACGTGT	ATCGTTTTGC	4380
TCACAAAACA	CACTTTAAAA	AAAAAATAAC	TTGTGCATCC	AGCCCAAATG	CACTGCTTCT	4440
TAAGTGGGGC	GATTTTGTTT	CCAATCAGTA	TCTGGCAATG	TCTGGAGGCA	TTTTGGTTGT	4500
CATACTGTGT	GTGTGGGTGT	GCCTGCTGGC	ATCCAGTGGG	CAGAGGCCAG	GGACACTGCT	4560
CAGCATGGTA	CAGTGCACAG	GACAGCCCCA	TCATCAAAGA	ATTATCTGGT	CCCAAATGTC	4620
AATAGTTTGA	GCATTGAGAG	ACCCTAGCCT	TCACTTAAGT	TTTTCTGGCG	TTCCTGATCT	4680
TTTTCTGTAG	TGAATTTCTA	GTGGCCATAA	AAGGTACTGG	GAGTGATCAA	CTAGAGCCAG	4740
GAATATTATT	TGGGCAGCCG	TTTGGTGCTG	TCCAAAACCT	TGTCCTTTCT	GTCTGGCAAG	4800
CTAGTATCCA	TTTATAGGTA	CCTCAGGAAC	CCAAATGATT	TGTCATAAAA	TACAAGGAAT	4860
GTGAGCACAC	TGAAGACATT	TTTAAGAAGG	CTCATTTGCT	CAGCAGAATT	TTCAGTGATC	4920
TAGTGGCATT	TATAGAAAAG	GAAGGTGATC	ACTGAAGGCA	TGCTCACATA	ATATTCCTGA	4980
GCCCTGGTGG	GCGTTATCTA	GGGCAAAGGA	TTCCACCTGT	GTTTGGAGTT	GCGCCCATCC	5040
TCACTGTAGC	CAGAGCTTCT	CCTATCAGAG	TTTAGTATTT	TGTTTGAATA	GAGGATCTTG	5100
CTGCTTAAAA	CAGTTGAAAA	GACCCTGATG	GGCAGGCCGT	AATTGACAAG	CGAATGATGG	5160

GAACATGAAT	CGGTCTTAGG	GAAGCATCTG	TCAAAGTGGT	CCTTG GTTAA	AACAAGTGCC	5220
TCCTCCTCTC	AGTGTCACCT	GATTGTGTGC	TTGAATTCTT	CGGAAACTG	GGTGTATGAG	5280
ACCCACGATG	AATTTGCCCA	CACGATTGAT	TGGACTCTTC	CTTCACCTGC	TCTTCAGCCA	5340
GTGCCAGTTC	CTTTTCTGAT	CATGTGATTG	ACGTGAGAAC	TGTAGTCTGT	ATATCAAATC	5400
TTTAGAATGT	TTTTGAGTTT	CCTGGGACAC	AGGAAACCCA	GCACTTAGCA	TACTACAAAT	5460
CTAATGTCTT	AATGGCATCA	TAAAAAGAGG	CTTTAAACAC	AGACTCCAGT	TAGCTAAGTG	5520
GTTTCTGCTA	GTGCCGGTAC	TGTTGCAGGG	GCCCTGTGAG	ATGCCCCAGT	TCCCTGAAAG	5580
AAATGAAAAG	GCCAGTTACC	GGTAGGTGGT	GTGGAAAACA	TGGGCTAGAT	CATCAGGCAG	5640
GACAGAATGC	CTGGCTGTGG	GTGGGAGCAC	CCCAGCTTGG	CGTTGAGTTC	TGGTTCCTACC	5700
ACTGCGTTGT	TTTGTGACCA	ATTATGAGTT	GCTTAACCTT	TCTTTGCTAC	TATTTCCCTG	5760
TTTGCAAAAT	GGTTCATTGA	CCCCTGTCTT	CCACCTCCCA	AGGACAATTT	CAACAGCCTA	5820
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AAGAGCAGGA	ACCAGGTAGA	TGTGGAAATG	TCATGTCTTT	TGTTCTAAAG	AAAAGGCATT	5940
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AAATTGCAAC	AACGCCCAGT	TATAAACCCA	GCTAGTTTGG	GTATGATTGT	AAGAAAAAAA	6060
AGCTGGCCAT	TCTGTATTTG	GGGAATTGAT	TTTCCTAAAC	TTATATTATC	TTAGTAGTCT	6120
AGATTTATCA	TATTGTACTA	TCATCCTGGC	TTTTTTAAGA	CTTAAGAAGA	TCAAGTAAAT	6180
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GGGTGGTATT	TTAACGGCAG	CACCTCTGAT	TGTCTTTTGG	AGGGCTGGTG	TGTGTTTGAA	6360
GTTCTGTCCT	CCTTCCAGTG	GACTCTAACT	TCTCCTGATG	CACGTGAGAC	ACATTGTCCT	6420
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ATCTCTTTTG	CCCACATGAG	TGTTTGTGGA	CAATACAGCC	TGCTTTCCAA	AACTTTGCTA	6540
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TGCTCAGAGA	CACTGAGAAC	CGGAAGCTGC	CCGGGCAATT	CAGTCTATGA	AATGATCTTT	6840
CTTGTGATTA	AGGCAAACGA	AGAACTGAAT	GTTTAATAGT	GTA CTCTGCT	GTACCCAGAA	6900
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TACCTTCTTA	TATAAATATT	TTTGTTTTTC	CTTTAAGATA	AAAATGATGA	TGGAGGAAAA	7140
ATAAAACATC	TTACATCTTC	AAGAGAGTGT	AGTTATTGTG	GAAAGTTTTT	CCGTTCAAAT	7200

TATTACCTCA	ATATTCATCT	CAGAACGCAT	ACAGGTAAAG	AACTTTTATT	TTTTTAACCA	7260
TGCATTAGTT	AAATTATGTA	GTTATCTAAT	TTTTTTGTTG	TTGTTGTTCA	GATACTCTGC	7320
CAGATCCTTG	GACTAGCTTA	AGGATAAATA	TGTAGCATGT	TGATTGCAGT	GGTTATTTTT	7380
ATTCTTTTAT	TGCCATTGTA	ACTTGAGCCA	TTGTTCTTAT	TTGCAGTTCA	TTTCTTTTCT	7440
TTCTTTTTTG	TTTTTTGAGA	CGGAGTCTTG	CTCTGTCAAC	TCGGCTGGAG	TGCAGTGGTG	7500
CAATTTTCGGC	TCACTGCAGC	CTCCACCTCC	CTGGTTCAAG	CAATACTCCT	GCCTCAGCCT	7560
CCCCAGTAGT	TGGGATTACA	GGTACCTGCC	ACCACACCCG	GCTAATTTCT	GTATTTTTTAG	7620
TAGAGATGGG	GTTTCACCAT	GCTGGCCAGG	CTGGTTTCGA	ACTCCTGACC	TCAAGTGATC	7680
CGCTCACCTT	GGCCTCCCAT	AGTGTGGGCC	TCCCATAGTG	CTGGGATTAC	AGGCGTGAGC	7740
CACCGCGCCC	GGACAAAGTT	CATTTGTTTA	GTTTATGACT	GCTATGTCCT	GACTCTTATC	7800
TTATTAAAAG	CTACAGTATT	TTAAAATGCT	GCATCTTATG	TCTTTATGAT	TGAGAATGAA	7860
ATGAGAATCT	ATTTAGTAGT	CTTGAGATTG	TGAAAGGAGC	TATGACATCA	TGATGTAGGA	7920
GGCTGCGTAG	ATTTGAAATT	TCATCTCTTC	CACTTACTAT	CTGTGCACCC	TTGGGCAAGT	7980
TATTTAACCT	TTTTGTGCTT	TTAGTTTTCT	TTGCTGTAAA	AGTAGAATAA	TACATATTTT	8040
CCTAGGGCTG	TTAGGAAGAT	TAAATAAGTT	AGAAGTGTTG	CTGTTAATTT	TTCTATTGAA	8100
GATAGGCATT	CATAATTTCA	AATATTCATT	ACAGTAAGGA	TGATAAAGAA	CTGATGAGAA	8160
ATCCTATGTG	ATAGTAGATC	GAGAAAGCAA	AAGGAGGAAA	GAAGCCTGTT	TTCTTAATAA	8220
ATAGATATTT	GATCTATTTT	AGTGCTTTTC	ATACACTTCT	ATAATAAAGT	GCCATTTCTT	8280
GCCTTAGGTG	AAAAACCATA	CAAATGTGAA	TTTTGTGAAT	ATGCTGCAGC	CCAGAAGACA	8340
TCTCTGAGGT	ATCACTTGGA	GAGACATCAC	AAGGAAAAAC	AAACCGATGT	TGCTGCTGAA	8400
GTCAAGAACG	ATGGTAAAAA	TCAGGACACT	GAAGATGCAC	TATTAACCGC	TGACAGTGCG	8460
CAAACCAAAA	ATTTGAAAAG	ATTTTTTGAT	GGTGCCAAAG	ATGTTACAGG	CAGTCCACCT	8520
GCAAAGCAGC	TTAAGGAGAT	GCCTTCTGTT	TTTCAGAATG	TTCTGGGCAG	CGCTGTCCTC	8580
TCACCAGCAC	ACAAAGATAC	TCAGGATTTT	CATAAAAATG	CAGCTGATGA	CAGTGCTGAT	8640
AAAGTGAATA	AAAACCCTAC	CCCTGCTTAC	CTGGACCTGT	TAAAAAAGAG	ATCAGCAGTT	8700
GAAACTCAGG	CAAATAACCT	CATCTGTAGA	ACCAAGGCGG	ATGTTACTCC	TCCTCCGGAT	8760
GGCAGTACCA	CCCATAACCT	TGAAGTTAGC	CCCAAAGAGA	AGCAAACGGA	GACCGCAGCT	8820
GACTGCAGAT	ACAGGCCAAG	TGTGGATTGT	CACGAAAAAC	CTTTAAATTT	ATCCGTGGGG	8880
GCTCTTCACA	ATTGCCCGGC	AATTTCTTTG	AGTAAAAGTT	TGATTCCAAG	TATCACCTGT	8940
CCATTTTGTA	CCTTCAAGAC	ATTTTATCCA	GAAGTTTTAA	TGATGCACCA	GAGACTGGAG	9000
CATAAATACA	ATCCTGACGT	TCATAAAAAC	TGTCGAAACA	AGTCCTTGCT	TAGAAGTCGA	9060
CGTACCGGAT	GCCCGCCAGC	GTTGCTGGGA	AAAGATGTGC	CTCCCCCTCC	TAGTTTCTGT	9120
AAACCCAAGC	CCAAGTCTGC	TTTCCCGGCG	CAGTCCAAAT	CCCTGCCATC	TGCGAAGGGG	9180
AAGCAGAGCC	CTCCTGGGCC	AGGCAAGGCC	CCTCTGACTT	CAGGGATAGA	CTCTAGCACT	9240

TTAGCCCCAA	GTAACCTGAA	GTCCCACAGA	CCACAGCAGA	ATGTGGGGGT	CCAAGGGGCC	9300
GCCACCAGGC	AACAGCAATC	TGAGATGTTT	CCTAAAACCA	GTGTTTCCCC	TGCACCGGAT	9360
AAGACAAAAA	GACCCGAGAC	AAAATTGAAA	CCTCTTCCAG	TAGCTCCTTC	TCAGCCCACC	9420
CTCGGCAGCA	GTAACATCAA	TGGTTCCATC	GACTACCCCG	CCAAGAACGA	CAGCCCGTGG	9480
GCACCTCCGG	GAAGAGACTA	TTTCTGTAAT	CGGAGTGCCA	GCAATACTGC	AGCAGAATTT	9540
GGTGAGCCCC	TTCCAAAAAG	ACTGAAGTCC	AGCGTG GTTG	CCCTTGACGT	TGACCAGCCC	9600
GGGGCCAATT	ACAGAAGAGG	CTATGACCTT	CCCAAGTACC	ATATGGTCAG	AGGCATCACA	9660
TCACTGTTAC	CGCAGGACTG	TGTGTATCCG	TCGCAGGCGC	TGCCTCCCAA	ACCAAGGTTC	9720
CTGAGCTCCA	GCGAGGTCGA	TTCTCCAAAT	GTGCTGACTG	TTCAGAAGCC	CTATGGTGGC	9780
TCCGGGCCAC	TTTACACTTG	TGTGCCTGCT	GGTAGTCCAG	CATCCAGCTC	GACGTTAGAA	9840
GGTATTGCAT	GAGGGGCGTC	GTGTTTAAAT	GGCTGCCTAC	AGTGATTAAT	AGCTAATCCA	9900
GGCATTCTCA	GTGGAGATGG	TACCACTCCC	AAGGGTGGGG	GGTAGGCAGC	CAGAAGTTCT	9960
TGGGGGTAC	AGAGAGAAGC	ATTCTTAGAT	ACGGCAGTGG	TTTGTGGTCC	TCCAAGGCTT	10020
ACTTAACTCT	GTGGGTTTAA	CTCTTAACCC	TGTGTATTTT	ATTCTTTTGA	TTTGTTTAGT	10080
CTTACTTTAT	TTTTAGAGAA	AGGGTCTTGC	TCCGTCATCT	AGATTGGAGT	GCAGCGGTGT	10140
AATCATAGCT	TACTGTAGTC	TTGAATTCCT	GAGTTCAAGA	GATCCTTCTG	CCTCAGCTTC	10200
CCAGGTAGCT	GAGACTATAT	GTGCTGCTAC	CATGCACAGC	TGATTTTTTAA	ATTTTTTTTTG	10260
TAGAGATGGA	GTTGCCCAGG	CTGGTCTTGA	ACTCCTGGCC	TGAGGTGATC	CTCCTGCGTT	10320
GACCTCCCAA	GTATCTTAGA	CTACAGATGC	ACTCCACCAC	GCTTG		10365

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3186
- (D) OTHER INFORMATION: /note= "ZABC1 Open Reading Frame"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCAATCGA	AAGTGACAGG	AAACATGCCA	ACTCAATCCC	TCTTAATGTA	CATGGATGGG	60
CCAGAAGTGA	TTGGCAGCTC	TCTTGGCAGT	CCGATGGAGA	TGGAGGATGC	CTTGTC AATG	120
AAAGGGACCG	CTGTTGTTCC	ATTCCGAGCT	ACACAAGAAA	AAAATGTCAT	CCAAATCGAG	180
GGGTATATGC	CCTTGGATTG	CATGTTCTGC	AGCCAGACCT	TCACACATTC	AGAAGACCTT	240
AATAAACATG	TCTTAATGCA	ACACCGGCCT	ACCCTCTGTG	AACCAGCAGT	TCTTCGGGTT	300



GAAGCAGAGT	ATCTCAGTCC	GCTTGATAAA	AGTCAAGTGC	GAACAGAACC	TCCCAAGGAA	360
AAGAATTGCA	AGGAAAATGA	ATTTAGCTGT	GAGGTATGTG	GGCAGACATT	TAGAGTCGCT	420
TTTGATGTTG	AGATCCACAT	GAGAACACAC	AAAGATTCTT	TCACTTACGG	GTGTAACATG	480
TGCGGAAGAA	GMTTSRRSSA	GCCTTGGTTT	CTTAAAAATC	ACATGCGGAC	ACATAATGGC	540
AAATCGGGGG	CCAGAAGCAA	ACTGCAGCAA	GGCTTGGAGA	GTAGTCCAGC	AACGATCAAC	600
GAGGTGCTCC	AGGTGCACGC	GGCCGAGAGC	ATCTCCTCTC	CTTACAAAAT	CTGCATGGTT	660
TGTGGCTTCC	TATTTCCAAA	TAAAGAAAGT	CTAATTGAGC	ACCGCAAGGT	GCACACCAAA	720
AAAAC TGCTT	TCGGTACCAG	CAGCGCGCAG	ACAGACTCTC	CACAAGGAGG	AATGCCGTCC	780
TCGAGGGAGG	ACTTCCTGCA	GTTGTTCAAC	TTGAGACCAA	AATCTCACCC	TGAAACGGGG	840
AAGAAGCCTG	TCAGATGCAT	CCCTCAGCTC	GATCCGTTCA	CCACCTTCCA	GGCTTGGCAG	900
CTGGCTACCA	AAGGAAAAGT	TGCCATTTGC	CAAGAAGTGA	AGGAATCGGG	GCAAGAAGGG	960
AGCACCGACA	ACGACGATTC	GAGTTCCGAG	AAGGAGCTTG	GAGAAACAAA	TAAGGGCAGT	1020
TGTGCAGGCC	TCTCGCAAGA	GAAAGAGAAG	TGCAAAACT	CCCACGGCGA	AGCGCCCTCC	1080
GTGGACGCGG	ATCCCAAGTT	ACCCAGTAGC	AAGGAGAAGC	CCACTCACTG	CTCCGAGTGC	1140
GGCAAAGCTT	TCAGAACCTA	CCACCAGCTG	GTCTTGCACT	CCAGGGTCCA	CAAGAAGGAC	1200
CGGAGGGCCG	GCGCGGAGTC	GCCCACCATG	TCTGTGGACG	GGAGGCAGCC	GGGGACGTGT	1260
TCTCCTGACC	TCGCCGCCCC	TCTGGATGAA	AATGGAGCCG	TGGATCGAGG	GGAAGGTGGT	1320
TCTGAAGACG	GATCTGAGGA	TGGGCTTCCC	GAAGGAATCC	ATCTGGATAA	AAATGATGAT	1380
GGAGGAAAAA	TAAACATCT	TACATCTTCA	AGAGAGTGTA	GTTATTGTGG	AAAGTTTTTC	1440
CGTTCAAATT	ATTACCTCAA	TATTCATCTC	AGAACGCATA	CAGGTGAAAA	ACCATACAAA	1500
TGTGAATTTT	GTGAATATGC	TGCAGCCAG	AAGACATCTC	TGAGGTATCA	CTTGGAGAGA	1560
CATCACAAGG	AAAAACAAAC	CGATGTTGCT	GCTGAAGTCA	AGAACGATGG	TAAAAATCAG	1620
GACACTGAAG	ATGCACTATT	AACCGCTGAC	AGTGCGCAAA	CCAAAAATTT	GAAAAGATTT	1680
TTTGATGGTG	CCAAAGATGT	TACAGGCAGT	CCACCTGCAA	AGCAGCTTAA	GGAGATGCCT	1740
TCTGTTTTTC	AGAATGTTCT	GGGCAGCGCT	GTCCTCTCAC	CAGCACACAA	AGATACTCAG	1800
GATTTCCATA	AAAATGCAGC	TGATGACAGT	GCTGATAAAG	TGAATAAAAA	CCCTACCCCT	1860
GCTTACCTGG	ACCTGTTAAA	AAAGAGATCA	GCAGTTGAAA	CTCAGGCAAA	TAACCTCATC	1920
TGTAGAACCA	AGGCGGATGT	TACTCCTCCT	CCGGATGGCA	GTACCACCCA	TAACCTTGAA	1980
GTTAGCCCCA	AAGAGAAGCA	AACGGAGACC	GCAGCTGACT	GCAGATACAG	GCCAAGTGTG	2040
GATTGTCACG	AAAAACCTTT	AAATTTATCC	GTGGGGGCTC	TTCACAATTG	CCCGGCAATT	2100
TCTTTGAGTA	AAAGTTTGAT	TCCAAGTATC	ACCTGTCCAT	TTTGTACCTT	CAAGACATTT	2160
TATCCAGAAG	TTTTAATGAT	GCACCAGAGA	CTGGAGCATA	AATACAATCC	TGACGTTCAT	2220
AAAAC TGTC	GAAACAAGTC	CTTGCTTAGA	AGTCGACGTA	CCGGATGCCC	GCCAGCGTTG	2280
CTGGGAAAAG	ATGTGCCTCC	CCTCTCTAGT	TTCTGTAAAC	CCAAGCCCAA	GTCTGCTTTC	2340

```

CCGGCGCAGT CCAAATCCCT GCCATCTGCG AAGGGGAAGC AGAGCCCTCC TGGGCCAGGC      2400
AAGGCCCCCTC TGACTTCAGG GATAGACTCT AGCACTTTAG CCCCAGTAA CCTGAAGTCC      2460
CACAGACCAC AGCAGAAATGT GGGGGTCCAA GGGGCCGCCA CCAGGCAACA GCAATCTGAG      2520
ATGTTTCCTA AAACCAAGTGT TTCCCCTGCA CCGGATAAGA CAAAAAGACC CGAGACAAAA      2580
TTGAAACCTC TTCCAGTAGC TCCTTCTCAG CCCACCCTCG GCAGCAGTAA CATCAATGGT      2640
TCCATCGACT ACCCCGCCAA GAACGACAGC CCGTGGGCAC CTCCGGGAAG AGACTATTTT      2700
TGTAATCGGA GTGCCAGCAA TACTGCAGCA GAATTTGGTG AGCCCCTTCC AAAAAGACTG      2760
AAGTCCAGCG TGGTTGCCCT TGACGTTGAC CAGCCCGGGG CCAATTACAG AAGAGGCTAT      2820
GACCTTCCCA AGTACCATAT GGTCAGAGGC ATCACATCAC TGTTACCGCA GGACTGTGTG      2880
TATCCGTCGC AGGCGCTGCC TCCCAAACCA AGGTTCTCTGA GCTCCAGCGA GGTCGATTCT      2940
CCAAATGTGC TGACTGTTCA GAAGCCCTAT GGTGGCTCCG GGCCACTTTA CACTTGTGTG      3000
CCTGCTGGTA GTCCAGCATC CAGCTCGACG TTAGAAGGTC TTGGTGGATG TCAGTGCTTA      3060
CTCCCCATGA AATTAAATTT TACTTCATCC TTTGAGAAGC GAATGGTGAA AGCTACTGAA      3120
ATAAGCTGTG ATTGTACTGT ACATAAAACA TATGAGGAAT CTGCAAGGAA CACTACAGTT      3180
GTGTAA                                         3186

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## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1061
- (D) OTHER INFORMATION: /note= "ZABC1 Protein"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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Met Gln Ser Lys Val Thr Gly Asn Met Pro Thr Gln Ser Leu Leu Met
1           5           10           15
Tyr Met Asp Gly Pro Glu Val Ile Gly Ser Ser Leu Gly Ser Pro Met
20          25          30
Glu Met Glu Asp Ala Leu Ser Met Lys Gly Thr Ala Val Val Pro Phe
35          40          45
Arg Ala Thr Gln Glu Lys Asn Val Ile Gln Ile Glu Gly Tyr Met Pro
50          55          60
Leu Asp Cys Met Phe Cys Ser Gln Thr Phe Thr His Ser Glu Asp Leu
65          70          75          80
Asn Lys His Val Leu Met Gln His Arg Pro Thr Leu Cys Glu Pro Ala
85          90          95

```

Val	Leu	Arg	Val	Glu	Ala	Glu	Tyr	Leu	Ser	Pro	Leu	Asp	Lys	Ser	Gln
			100					105					110		
Val	Arg	Thr	Glu	Pro	Pro	Lys	Glu	Lys	Asn	Cys	Lys	Glu	Asn	Glu	Phe
		115					120					125			
Ser	Cys	Glu	Val	Cys	Gly	Gln	Thr	Phe	Arg	Val	Ala	Phe	Asp	Val	Glu
	130					135					140				
Ile	His	Met	Arg	Thr	His	Lys	Asp	Ser	Phe	Thr	Tyr	Gly	Cys	Asn	Met
145					150					155					160
Cys	Gly	Arg	Xaa	Xaa	Xaa	Xaa	Pro	Trp	Phe	Leu	Lys	Asn	His	Met	Arg
			165						170					175	
Thr	His	Asn	Gly	Lys	Ser	Gly	Ala	Arg	Ser	Lys	Leu	Gln	Gln	Gly	Leu
			180					185					190		
Glu	Ser	Ser	Pro	Ala	Thr	Ile	Asn	Glu	Val	Val	Gln	Val	His	Ala	Ala
		195					200					205			
Glu	Ser	Ile	Ser	Ser	Pro	Tyr	Lys	Ile	Cys	Met	Val	Cys	Gly	Phe	Leu
	210					215					220				
Phe	Pro	Asn	Lys	Glu	Ser	Leu	Ile	Glu	His	Arg	Lys	Val	His	Thr	Lys
225					230					235					240
Lys	Thr	Ala	Phe	Gly	Thr	Ser	Ser	Ala	Gln	Thr	Asp	Ser	Pro	Gln	Gly
				245					250					255	
Gly	Met	Pro	Ser	Ser	Arg	Glu	Asp	Phe	Leu	Gln	Leu	Phe	Asn	Leu	Arg
			260					265					270		
Pro	Lys	Ser	His	Pro	Glu	Thr	Gly	Lys	Lys	Pro	Val	Arg	Cys	Ile	Pro
		275					280					285			
Gln	Leu	Asp	Pro	Phe	Thr	Thr	Phe	Gln	Ala	Trp	Gln	Leu	Ala	Thr	Lys
	290					295					300				
Gly	Lys	Val	Ala	Ile	Cys	Gln	Glu	Val	Lys	Glu	Ser	Gly	Gln	Glu	Gly
305					310					315					320
Ser	Thr	Asp	Asn	Asp	Asp	Ser	Ser	Ser	Glu	Lys	Glu	Leu	Gly	Glu	Thr
				325					330					335	
Asn	Lys	Gly	Ser	Cys	Ala	Gly	Leu	Ser	Gln	Glu	Lys	Glu	Lys	Cys	Lys
			340					345					350		
His	Ser	His	Gly	Glu	Ala	Pro	Ser	Val	Asp	Ala	Asp	Pro	Lys	Leu	Pro
		355					360					365			
Ser	Ser	Lys	Glu	Lys	Pro	Thr	His	Cys	Ser	Glu	Cys	Gly	Lys	Ala	Phe
	370					375					380				
Arg	Thr	Tyr	His	Gln	Leu	Val	Leu	His	Ser	Arg	Val	His	Lys	Lys	Asp
385					390					395					400
Arg	Arg	Ala	Gly	Ala	Glu	Ser	Pro	Thr	Met	Ser	Val	Asp	Gly	Arg	Gln
				405					410					415	
Pro	Gly	Thr	Cys	Ser	Pro	Asp	Leu	Ala	Ala	Pro	Leu	Asp	Glu	Asn	Gly
			420					425					430		
Ala	Val	Asp	Arg	Gly	Glu	Gly	Gly	Ser	Glu	Asp	Gly	Ser	Glu	Asp	Gly
		435					440					445			

Leu Pro Glu Gly Ile His Leu Asp Lys Asn Asp Asp Gly Gly Lys Ile  
 450 455 460  
 Lys His Leu Thr Ser Ser Arg Glu Cys Ser Tyr Cys Gly Lys Phe Phe  
 465 470 475 480  
 Arg Ser Asn Tyr Tyr Leu Asn Ile His Leu Arg Thr His Thr Gly Glu  
 485 490 495  
 Lys Pro Tyr Lys Cys Glu Phe Cys Glu Tyr Ala Ala Ala Gln Lys Thr  
 500 505 510  
 Ser Leu Arg Tyr His Leu Glu Arg His His Lys Glu Lys Gln Thr Asp  
 515 520 525  
 Val Ala Ala Glu Val Lys Asn Asp Gly Lys Asn Gln Asp Thr Glu Asp  
 530 535 540  
 Ala Leu Leu Thr Ala Asp Ser Ala Gln Thr Lys Asn Leu Lys Arg Phe  
 545 550 555 560  
 Phe Asp Gly Ala Lys Asp Val Thr Gly Ser Pro Pro Ala Lys Gln Leu  
 565 570 575  
 Lys Glu Met Pro Ser Val Phe Gln Asn Val Leu Gly Ser Ala Val Leu  
 580 585 590  
 Ser Pro Ala His Lys Asp Thr Gln Asp Phe His Lys Asn Ala Ala Asp  
 595 600 605  
 Asp Ser Ala Asp Lys Val Asn Lys Asn Pro Thr Pro Ala Tyr Leu Asp  
 610 615 620  
 Leu Leu Lys Lys Arg Ser Ala Val Glu Thr Gln Ala Asn Asn Leu Ile  
 625 630 635 640  
 Cys Arg Thr Lys Ala Asp Val Thr Pro Pro Pro Asp Gly Ser Thr Thr  
 645 650 655  
 His Asn Leu Glu Val Ser Pro Lys Glu Lys Gln Thr Glu Thr Ala Ala  
 660 665 670  
 Asp Cys Arg Tyr Arg Pro Ser Val Asp Cys His Glu Lys Pro Leu Asn  
 675 680 685  
 Leu Ser Val Gly Ala Leu His Asn Cys Pro Ala Ile Ser Leu Ser Lys  
 690 695 700  
 Ser Leu Ile Pro Ser Ile Thr Cys Pro Phe Cys Thr Phe Lys Thr Phe  
 705 710 715 720  
 Tyr Pro Glu Val Leu Met Met His Gln Arg Leu Glu His Lys Tyr Asn  
 725 730 735  
 Pro Asp Val His Lys Asn Cys Arg Asn Lys Ser Leu Leu Arg Ser Arg  
 740 745 750  
 Arg Thr Gly Cys Pro Pro Ala Leu Leu Gly Lys Asp Val Pro Pro Leu  
 755 760 765  
 Ser Ser Phe Cys Lys Pro Lys Pro Lys Ser Ala Phe Pro Ala Gln Ser  
 770 775 780  
 Lys Ser Leu Pro Ser Ala Lys Gly Lys Gln Ser Pro Pro Gly Pro Gly  
 785 790 795 800

Lys Ala Pro Leu Thr Ser Gly Ile Asp Ser Ser Thr Leu Ala Pro Ser  
 805 810 815  
 Asn Leu Lys Ser His Arg Pro Gln Gln Asn Val Gly Val Gln Gly Ala  
 820 825 830  
 Ala Thr Arg Gln Gln Gln Ser Glu Met Phe Pro Lys Thr Ser Val Ser  
 835 840 845  
 Pro Ala Pro Asp Lys Thr Lys Arg Pro Glu Thr Lys Leu Lys Pro Leu  
 850 855 860  
 Pro Val Ala Pro Ser Gln Pro Thr Leu Gly Ser Ser Asn Ile Asn Gly  
 865 870 875 880  
 Ser Ile Asp Tyr Pro Ala Lys Asn Asp Ser Pro Trp Ala Pro Pro Gly  
 885 890 895  
 Arg Asp Tyr Phe Cys Asn Arg Ser Ala Ser Asn Thr Ala Ala Glu Phe  
 900 905 910  
 Gly Glu Pro Leu Pro Lys Arg Leu Lys Ser Ser Val Val Ala Leu Asp  
 915 920 925  
 Val Asp Gln Pro Gly Ala Asn Tyr Arg Arg Gly Tyr Asp Leu Pro Lys  
 930 935 940  
 Tyr His Met Val Arg Gly Ile Thr Ser Leu Leu Pro Gln Asp Cys Val  
 945 950 955 960  
 Tyr Pro Ser Gln Ala Leu Pro Pro Lys Pro Arg Phe Leu Ser Ser Ser  
 965 970 975  
 Glu Val Asp Ser Pro Asn Val Leu Thr Val Gln Lys Pro Tyr Gly Gly  
 980 985 990  
 Ser Gly Pro Leu Tyr Thr Cys Val Pro Ala Gly Ser Pro Ala Ser Ser  
 995 1000 1005  
 Ser Thr Leu Glu Gly Leu Gly Gly Cys Gln Cys Leu Leu Pro Met Lys  
 1010 1015 1020  
 Leu Asn Phe Thr Ser Ser Phe Glu Lys Arg Met Val Lys Ala Thr Glu  
 1025 1030 1035 1040  
 Ile Ser Cys Asp Cys Thr Val His Lys Thr Tyr Glu Glu Ser Ala Arg  
 1045 1050 1055  
 Asn Thr Thr Val Val  
 1060

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3066 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3066
- (D) OTHER INFORMATION: /note= "1b1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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GAATTCGGCA CGAGGCTCCA CCGACAGCCA GGCCTGGGC AGCACGCACT GGAGACCCAG	180
GACCCTGTGC AGGAGCAGCT CCGGGTGACA CGAGGGGACT GAAGATACTC CCACAGGGGC	240
TCAGCAGGAG CAATGGGTAA CCAAATGAGT GTTCCCCAAA GAGTTGAAGA CCAAGAGAAT	300
GAACCAGAAG CAGAGACTTA CCAGGACAAC GCGTCTGCTC TGAACGGGGT TCCAGTGGTG	360
GTGTCGACCC ACACAGTTCA GCACTTAGAG GAAGTCGACT TGGGAATAAG TGTCAAGACG	420
GATAATGTGG CCACTTCTTC CCCCAGACA ACGGAGATAA GTGCTGTTGC GGATGCCAAC	480
GGAAAGAATC TTGGGAAAGA GGCCAAACCC GAGGCACCAG CTGCTAAATC TCGTTTTTTC	540
TTGATGCTCT CTCGGCCTGT ACCAGGACGT ACCGGAGACC AAGCCGCAGA TTCATCCCTT	600
GGATCAGTGA AGCTTGATGT CAGCTCCAAT AAAGCTCCAG CGAACAAAGA CCCAAGTGAG	660
AGCTGGACAC TTCCGGTGGC AGCTGGACCG GGGCAGGACA CAGATAAAAC CCCAGGGCAC	720
GCCCCGGCCC AAGACAAGGT CCTCTCTGCC GCCAGGGATC CCACGCTTCT CCCACCTGAG	780
ACAGGGGGAG CAGGAGGAGA AGCTCCCTCC AAGCCCAAGG ACTCCAGCTT TTTTGACAAA	840
TTCTTCAAGC TGGACAAGGG ACAGGAAAAG GTGCCAGGTG ACAGCCAACA GGAAGCCAAG	900
AGGGCAGAGC ATCAAGACAA GGTGGATGAG GTTCTTGCT TATCAGGGCA GTCCGATGAT	960
GTCCCTGCAG GGAAGGACAT AGTTGACGGC AAGGAAAAAG AAGGACAAGA ACTTGGAAC	1020
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GCAGCAGCTA TAGCAGAGAA TAATAATTCC ATCATGAGTT TCTTTAAAC TCTGGTTTCA	1140
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ACTTCAGCTG ACCTTAAGTC AGACAAAGCC AACTTTACAT CCCAGGAGAC CCAAGGGGCT	1260
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CCTGCGAAGG AAGGCACCAA GGAGAAATCA GGACCCACCT CTCTGCCTCT GGGCAAAC	1380
TTTTGGAAAA AGTCAGTTAA AGAGGACTCA GTCCCCACAG GTGCGGAGGA GAATGTGGTG	1440
TGTGAGTCAC CAGTAGAGAT TATAAAGTCC AAGGAAGTAG AATCAGCCTT ACAAACAGTG	1500
GACCTCAACG AAGGAGATGC TGCACCTGAA CCCACAGAAG CGAAACTCAA AAGAGAAGAA	1560
AGCAAACCAA GAACCTCTCT GATGGCGTTT CTCAGACAAA TGTCAGTGAA AGGGGATGGA	1620
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ACAGAAAAGA CTATCACACC GCCAGAGCCT GAACCAACAG GAGCACCACA GAAGGGTAAA	1740
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CAGGAAGCCA AAGAACCAGC CCAGTGCACA GAGCAGGCCA CGGTGGACAC GAACTCACTG	1860
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TTTAAAGGCC TGGGACCAAA GCGGATGTTG GATGCTCAAG TGCAAACAGA CCCAGTATCC	1980

ATCGGACCAG	TTGGCAAACC	CAAGTAAACA	AATCAGCACG	GTTCCCACCA	GGTTCTCCTG	2040
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GCCTGTAATC	TCAGCACTTT	GGGAGGCCGA	GGCAGGTGGA	TCACCTGAGG	TCAGGAGTTC	2400
AAGACTAGCC	TGGCCAACAT	CATGAAACCC	CGTCTCTACT	AAAAATACAA	AAATTAGCCA	2460
GGCATGGTGG	CACACACCTG	TAGTCCCAGC	TACTCGGGAG	CCCAACGCAC	GAGAACCCTG	2520
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TGCTGCTAGA	AGGAATTAAG	CGTTGTAGTA	AACGCGTGCT	CATCCTCTAA	GCTTGAAGAA	2700
GGGAGACGAA	AATCCATTTG	TTTAAATTCA	CATCTCAAGG	AGGGAGAACC	CGGGCTGTGT	2760
TGGGTGGTTG	CCAATTTCTT	AGAACGGAAT	GTGTGGGGTA	TAGAAAAAGG	AATGAATAAG	2820
CGTTGTTTTT	CAAATAGGGT	CCTTGTAAGT	TATTGATGAG	AGGGAAAAGA	TTGACTGGGG	2880
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TACAACCTAA	AAAAAAAAAA	AAAAAACTC	GAGACTAGTT	CTCTCTCTCT	CTCGTGCCGA	3000
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CCTATA						3066

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGGCATTGG TATCAGGTAG CTG

23

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTGGAGCAGA GAGGGGATTG TGTG

24

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATCCCCTCA AACCTGCTG CTAC

24

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGGAGCCTGA ACTTCTGCAA TC

22

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGGGATACC GACATTG

17

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGCACATAAA ACAGCCAGC

19



## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTGGAATCAA TGGAGCAAAA

20

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTTACCC AATGTGGTCC

20

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGGTGAACA CCAATAAATG G

21

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGCAAATAA AACCAATAAA CTCG

24

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAAGATCTGA CCCCCTCAAT C

21

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GACTTCTTCA GGAAAGAGAT CAGTG

25

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCCATGTACC CACCTGAAAA ATC

23

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCAGAACACC CGTGCAGAAAT TAAG

24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTAAAACTT GGTGCTTAAA TCTA

24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCTCACAAG GCAGATGTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTGTATG TTGAGCCATC

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTCCAATCT CATTCTATGA GG

22

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCTTGTTTAA GTGTCAC TAG GG

22

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CACTCTGGTA AATGACCTTT GTC

23

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTACACCAT TCCAAC TTTG G

21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCAGATGTA TGTTTGCTAC GGAAC

25

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCTCAAACCT GTCCACTTCT TG

22

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTGCTGTGGT GGAGAATGG

19

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTCCTCCTT CTCCCTCATC CTAC

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AATGCCTCCA CTCACAGGAA TG

22

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTCTTCAGT GTCTTCCTAT TGA

23

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGAGGAGGT TGTAGGCAAC

20

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGCAAAGCAA AGGTGGCACA C

21

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGACATGGGA GAAGACACAC TTCC

24

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGGTTTACCA ATGTGTTTGG

20

## (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCTACATCCC ATTCTCTTCT G